

## ***Supplementary Material***

**Dual RNA-seq analysis of *Trichophyton rubrum* and HaCat keratinocytes co-culture highlights important genes for fungal-host interactions**

**RUNNING TITLE: Dual RNA-seq of *T. rubrum*-keratinocyte interaction**

**AUTHORS:** Monise Fazolin Petrucelli<sup>1</sup>, Kamila Peronni<sup>4</sup>, Pablo Rodrigo Sanches<sup>6</sup>, Tatiana Takahasi Komoto<sup>1</sup>, Josie Budag Matsuda<sup>1</sup>, Rene Oliveira Beleboni<sup>1,2</sup>, Nilce Maria Martinez-Rossi<sup>6</sup>, Wilson Araújo da Silva Junior<sup>3,4,5</sup>, Mozart Marins<sup>1,2</sup>, Ana Lúcia Fachin<sup>1,2\*</sup>

<sup>1</sup> Biotechnology Unit, University of Ribeirão Preto-UNAERP, Brazil.

<sup>2</sup> Medicine School, University of Ribeirão Preto- UNAERP, Brazil

<sup>3</sup> Department of Genetics, Ribeirão Preto Medical School, and Center for Integrative System Biology - CISBi-NAP/USP, University of São Paulo, Ribeirão Preto, São Paulo, Brazil.

<sup>4</sup> National Institute of Science and Technology in Stem Cell and Cell Therapy and Center for Cell-Based Therapy, Ribeirão Preto, São Paulo, Brazil.

<sup>5</sup> Center for Medical Genomics at Clinical Hospital of the Medical School of Ribeirão Preto, University of São Paulo, Ribeirão Preto, SP, Brazil.

<sup>6</sup> Department of Genetics, Ribeirão Preto Medical School, University of São Paulo, Ribeirão Preto, Brazil

**\*Corresponding author:** Ana Lúcia Fachin – Biotechnology Unit, University of Ribeirão Preto. Av: Costáble Romano 2201, 14096-900, Ribeirão Preto, SP, Brazil FAX + 55 -16-36037030. email: afachin@unaerp.br

### **1 Supplementary Figures and Tables**

**Supplementary Figure S1: Distribution of differentially expressed genes after 24 h of co-culture.** The red points indicate differentially expressed genes.

**Supplementary Table S1: General features of dual RNA-seq sequences against reference genomes.** CBS I, CBS II, CBS III: *T. rubrum* libraries; CO I, CO II, CO III: co-culture libraries; H I, H II, H III: human keratinocyte libraries. The libraries were constructed in triplicate, with I, II and III corresponding to the sample number of each condition. PE: paired-end sequence; SR: single read sequence.

**Supplementary Table S2: Complete list of genes differentially expressed in keratinocytes after 24 h of co-culture.**

**Supplementary Table S3: Complete list of genes differentially expressed in *T. rubrum* after 24 h of co-culture.**

**Supplementary Table S4: Primers used for qPCR analysis.**